AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-45 (Canceled).

46 (Previously Presented). A method for reducing or eliminating the susceptibility of a tropoelastin to proteolysis comprising mutating a sub-sequence in the tropoelastin so that the susceptibility of the tropoelastin to proteolysis is reduced or eliminated.

47 (Previously Presented). A method according to claim 46 wherein one sub-sequence is mutated.

48 (Previously Presented). A method according to claim 46 wherein one amino acid residue in the sub-sequence is mutated.

49 (Previously Presented). A method according to claim 49 wherein the sub-sequence is capable of being digested by a serine protease.

50 (Currently Amended). A method according to claim 50 wherein the sub-sequence has an amino acid sequence including the sequence: RAAAG, aa 1 to 5 of SEQ ID NO:9.

51(Currently Amended). A method according to claim 50 wherein the subsequence is mutated by replacing arginine in the sequence: RAAAG, aa 1 to 5 of SEQ ID NO:9, with alanine.

52 (Previously Presented). A method according to claim 49 wherein the subsequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44.

53(Previously Presented). A method according to claim 52 wherein the subsequence is mutated by replacing arginine in the sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44 with alanine.

54 (Previously Presented). A method according to claim 49 wherein the subsequence is capable of being digested by thrombin and has an amino acid sequence shown in SEQ ID NOS: 8 or 9.

55 (Previously Presented). A method according to claim 49 wherein the subsequence is capable of being digested by plasmin and has an amino acid sequence shown in SEQ ID NOS: 11 or 12.

56 (Previously Presented). A method according to claim 49 wherein the subsequence is capable of being digested by kallikrein.

57 (Previously Presented). A method according to claim 56 wherein the subsequence has an amino acid sequence shown in SEQ ID NOS: 9 or 10.

58 (Previously Presented). A method according to claim 46 wherein the subsequence is capable of being digested by a metalloproteinase.

59 (Currently Amended). A method according to claim 58 wherein the subsequence has an amino acid sequence including the sequence: ALAAA, aa 1 to 5 of SEQ ID NO:13.

60 (Currently Amended). A method according to claim 59 wherein the subsequence is mutated by replacing alanine at any position in the sequence: ALAAA, aa 1 to 5 of SEQ ID NO:13, with another amino acid residue.

61 (Currently Amended). A method according to claim 60 wherein the subsequence is mutated by replacing the alanine which is N-terminal to leucine in the sequence: ALAAA, aa 1 to 5 of SEQ ID NO:13, with another amino acid.

62 (Previously Presented). A method according to claim 58 wherein the subsequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 45 to 70.

63 (Previously Presented). A method according to claim 61 wherein the subsequence is mutated by replacing alanine at any position in the sequence selected from the group of sequences shown in SEQ ID NOS: 45 to 70 with another amino acid residue.

64 (Previously Presented). A method according to claim 63 wherein the alanine that is replaced is N-terminal to leucine.

65 (Previously Presented). A method according to claim 58 wherein the subsequence is capable of being digested by gelatinase A or B.

66 (Previously Presented). A method according to claim 65 wherein the subsequence has an amino acid sequence shown in SEQ ID NO: 13.

67 (Previously Presented). A method according to any one of claims 46 to 66 wherein the tropoelastin is human tropoelastin.

68 (Previously Presented). A method for enhancing the susceptibility of a tropoelastin to proteolysis comprising inserting a sub-sequence into the tropoelastin so that the susceptibility of the tropoelastin to proteolysis is enhanced.

69 (Previously Presented). A method according to claim 68 wherein one sub-sequence is inserted.

70 (Previously Presented). A method according to claim 68 wherein the inserted sub-sequence is capable of being digested with a serine protease.

71 (Currently Amended). A method according to claim 70 wherein the inserted sub-sequence has an amino acid sequence including the sequence: RAAAG, aa 1 to 5 of SEQ ID NO:9.

72 (Previously Presented). A method according to claim 70 wherein the inserted sub-sequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44.

73 (Previously Presented). A method according to claim 70 wherein the inserted sub-sequence is capable of being digested by thrombin and has an amino acid sequence shown in SEQ ID NOS: 8 or 9.

74 (Previously Presented). A method according to claim 70 wherein the inserted sub-sequence is capable of being digested by plasmin and has an amino acid sequence shown in SEQ ID NOS: 11 or 12.

75 (Previously Presented). A method according to claim 70 wherein the inserted sub-sequence is capable of being digested by kallikrein.

76 (Previously Presented). A method according to claim 75 wherein the inserted sub-sequence has an amino acid sequence shown in SEQ ID NOS: 9 or 10.

77 (Previously Presented). A method according to claim 68 wherein the inserted sub-sequence is capable of being digested by a metalloproteinase.

78 (Currently Amended). A method according to claim 76 wherein the inserted sub-sequence has an amino acid sequence including the sequence: ALAAA, aa 1 to 5 of SEQ ID NO:13.

79 (Previously Presented). A method according to claim 77 wherein the inserted sub-sequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 45 to 70.

80 (Previously Presented). A method according to claim 77 wherein the inserted sub-sequence is capable of being digested by gelatinase A or B.

81 (Previously Presented). A method according to claim 80 wherein the inserted sub-sequence has the amino acid sequence shown in SEQ ID NO: 13.

82 (Previously Presented). A method according to any one of claims 68 to 81 wherein the tropoelastin is human tropoelastin.

83 (Currently Amended). A peptidomimetic molecule comprising all or part of a peptide selected from the group consisting of KAPGVGGAF, SEQ ID NO:9; RAAAGLG, SEQ ID NO:9; RSLSPELREGD, SEQ ID NO:10; KAAQFGLVPGV, SEQ

ID NO:14; KSAAKVAAKAQLRAA, 503 to 517 of SEQ ID NO:4; RSLSPELRE, 1 to 9 of SEQ ID NO:10; ~~AND~~ LAAAKAAKYGAA, 2 to 13 of SEQ ID NO:13.

84 (Currently Amended). A peptidomimetic molecule which has the sequence: H-Ala-Ala-Lys-Ala-Gln-Leu-Arg-Ala-Ala-Ala-Gly-Leu-Gly-Ala-OH, 509 to 522 of SEQ ID NO:4, or H-Ala-Ala-Lys-Ala-Gln-Leu-Arg-R-Ala-Ala-Ala-Gly-Leu-Gly-Ala-OH, 509 to 522 of SEQ ID NO:4, (where R = a reduced peptide bond).

85 (Currently Amended). A peptidomimetic molecule which is a retro-inverso pseudo peptide which has the sequence: H-D-Ala-Gly-D-Leu-Gly-D-Ala-D-Ala-D-Ala-(R)-D-Arg-D-Leu-D-Gln-D-Ala-D-Lys-D-Ala-D-Ala-OH , SEQ ID NO:84, (where R = a reduced peptide bond) or H-D-Ala-Gly-D-Leu-Gly-D-Ala-D-Ala-D-Ala-D-Arg-D-Leu-D-Gln-D-Ala-D-Lys-D-Ala-D-Ala-OH, SEQ ID NO: 85.

86 (Currently Amended). A peptidomimetic molecule which has the sequence H-Val-Pro-Gly-Ala-Leu-Ala-Ala-Ala-OH , 557 to 564 of SEQ ID NO:5, or H-Val-Pro-Gly-Ala-(R)-Leu-Ala-Ala-Ala-OH (where R = a reduced peptide bond), SEQ ID NO 86.

87 (Currently Amended). A peptidomimetic molecule which is a retro-inverso pseudo peptide which has the sequence: H-D-Ala-D-Ala-D-Ala-D-Leu-(R)-D-Ala-Gly-D-Pro-D-Val-OH (where R = a reduced peptide bond), SEQ ID NO:87 or H-D-Ala-D-Ala-D-Ala-D-Leu-D-Ala-Gly-D-Pro-D-Val-OH, SEQ ID NO:88.

88 (Previously Presented). A method for enhancing the purification of a tropoelastin comprising including a peptidomimetic molecule according to any one of claims 82 to 86 in a crude tropoelastin preparation which is being subjected to purification.

89 (Previously Presented). A pharmaceutical composition comprising a peptidomimetic molecule according to any one of claims 82 to 86 and a pharmaceutically acceptable carrier.